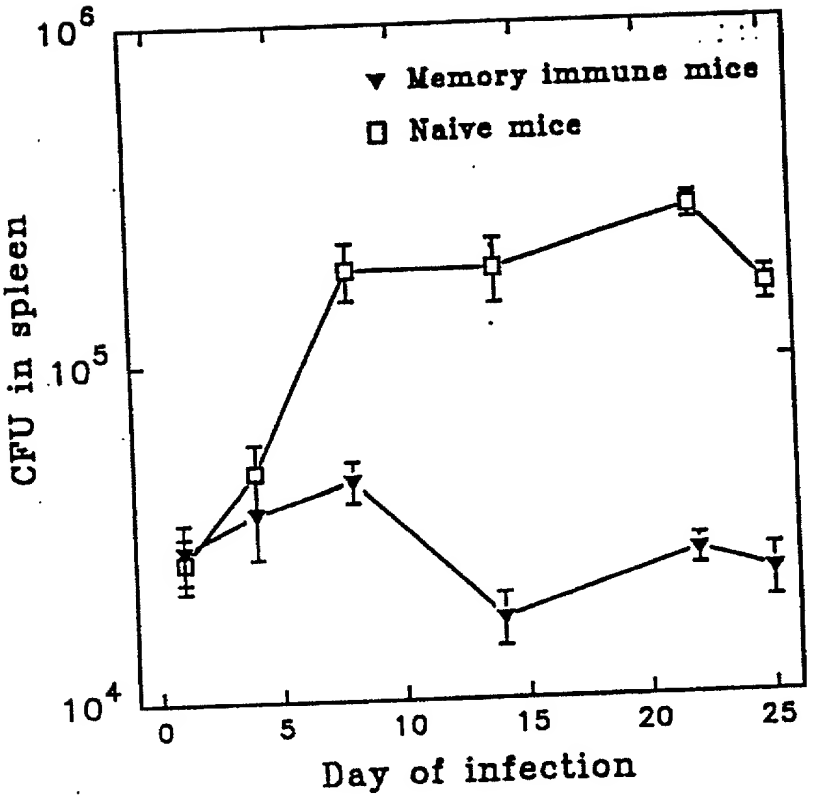

10^6
10^5
10^4
CFU in spleen
Memory immune mice
Naive mice
0
5
10
15
20
25
Day of infection

Fig. 1

Fig. 1

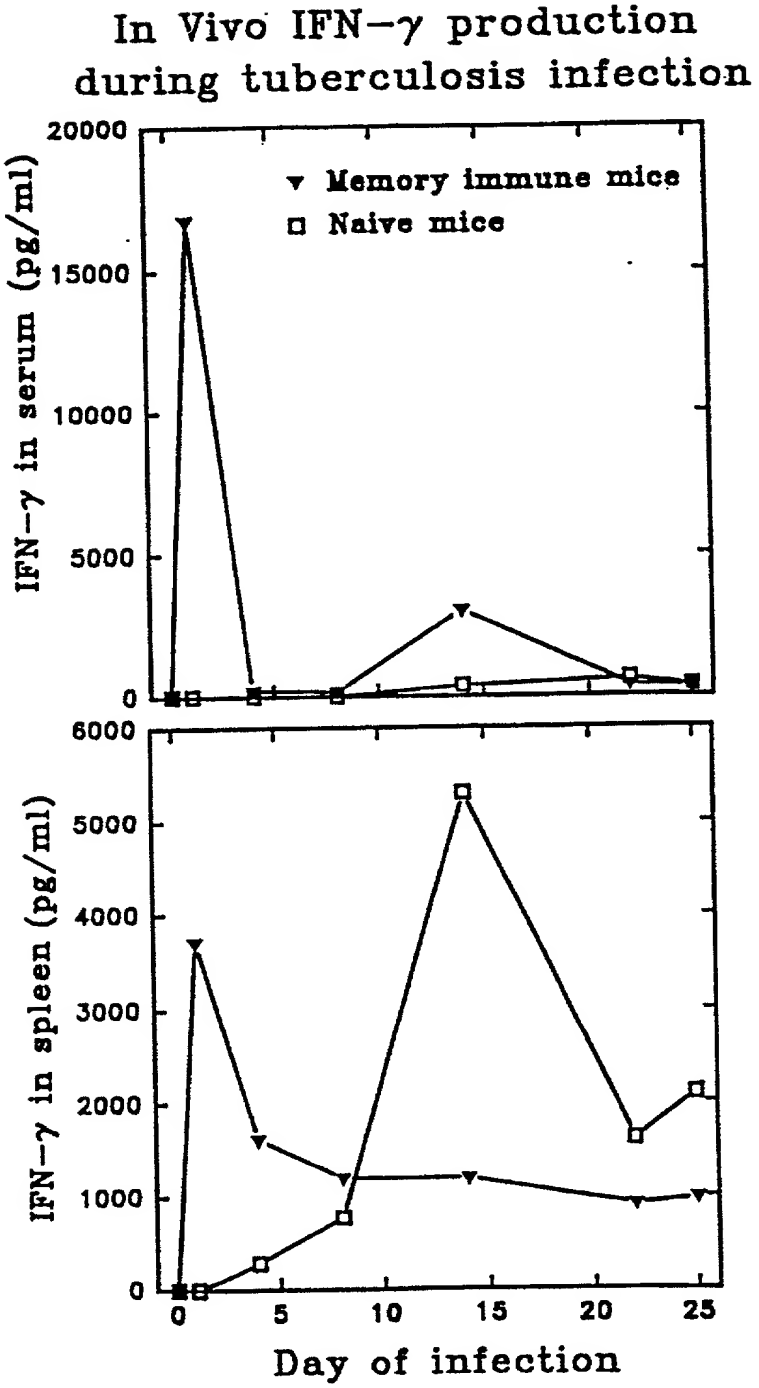

In Vivo IFN−γ production
during tuberculosis infection
Memory immune mice
Naive mice
IFN−γ in serum (pg/ml)
20000
15000
10000
5000
0
IFN−γ in spleen (pg/ml)
6000
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Day of infection

Fig. 2

In vitro response of spleen lymphocytes

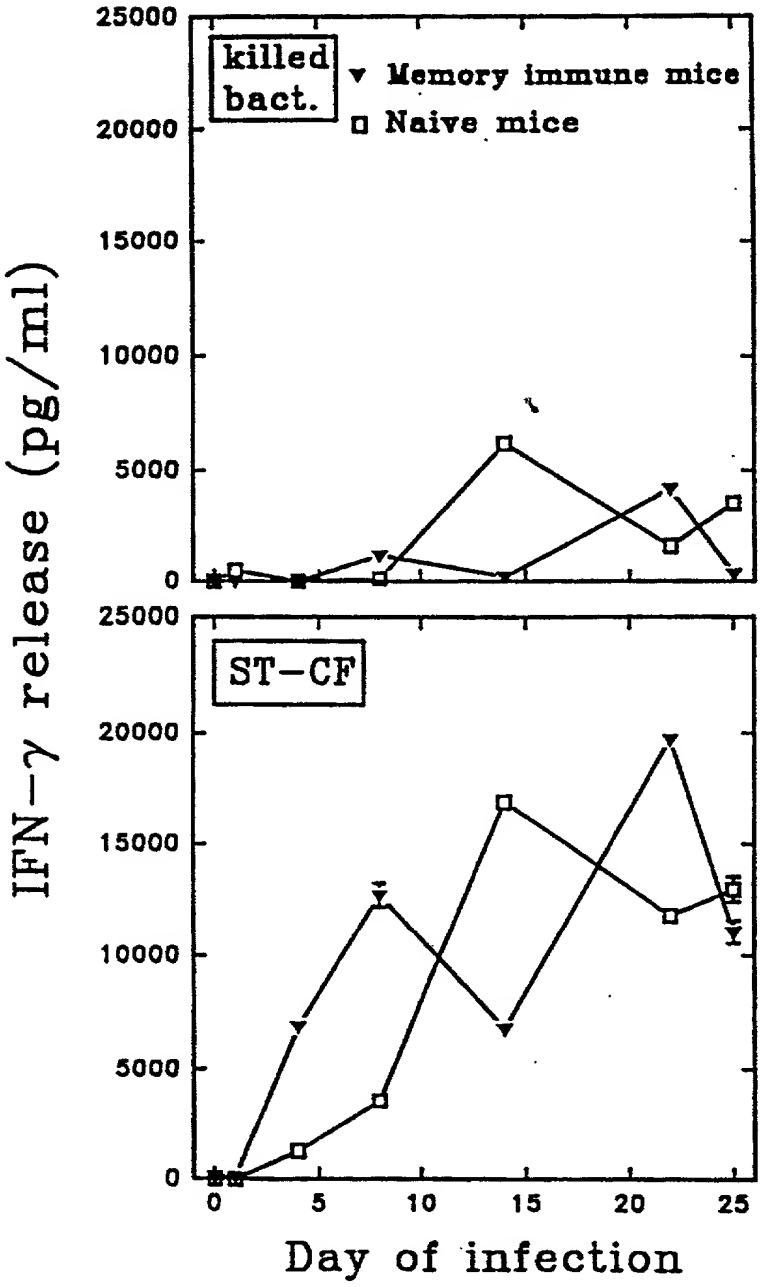


Fig. 3

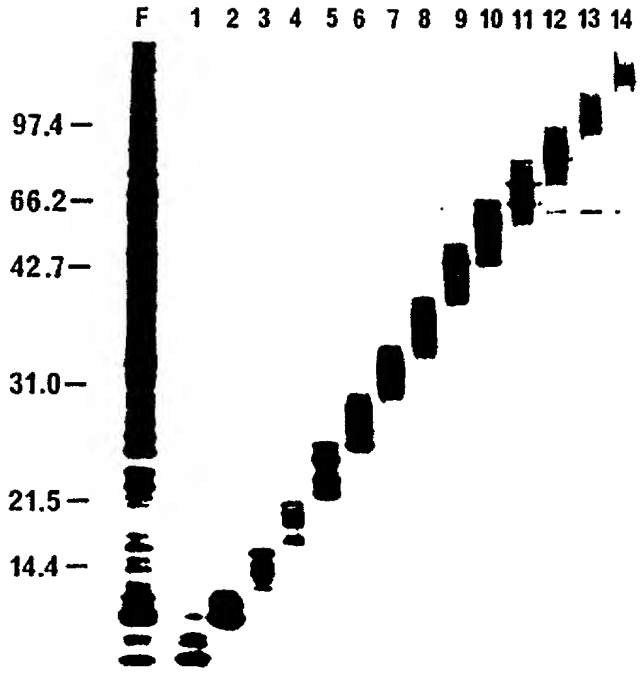


Fig. 4

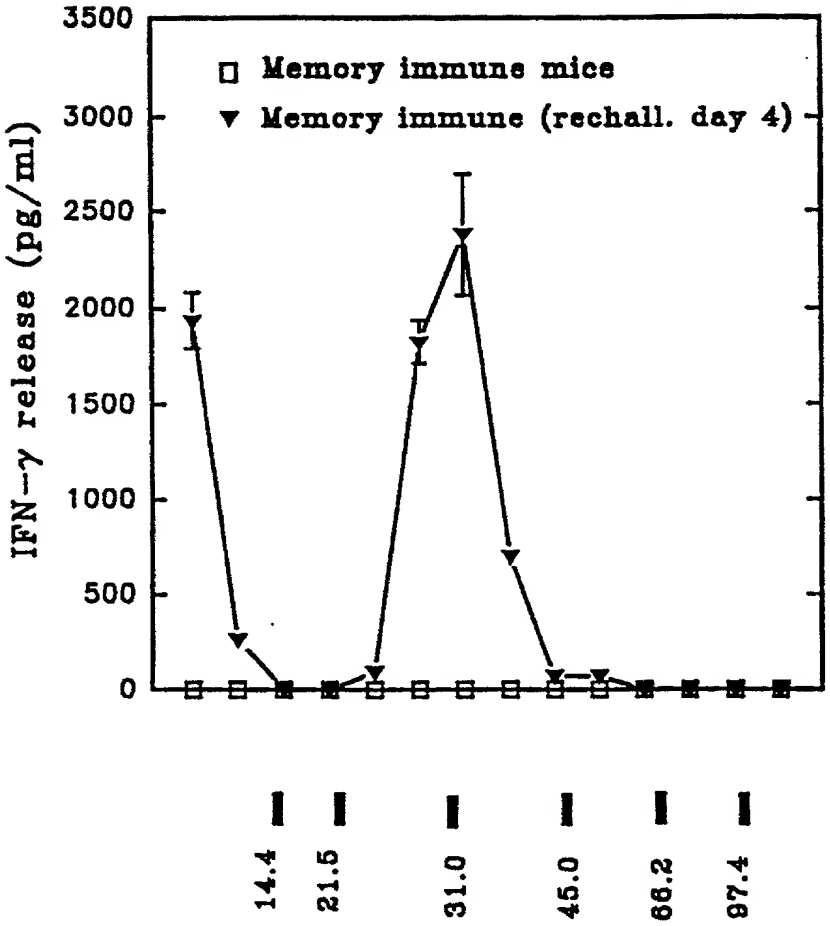

3500
3000
2500
2000
1500
1000
500
0
IFN-γ release (pg/ml)
Memory immune mice
Memory immune (rechall. day 4)
14.4
21.5
31.0
45.0
66.2
97.4

Fig. 5

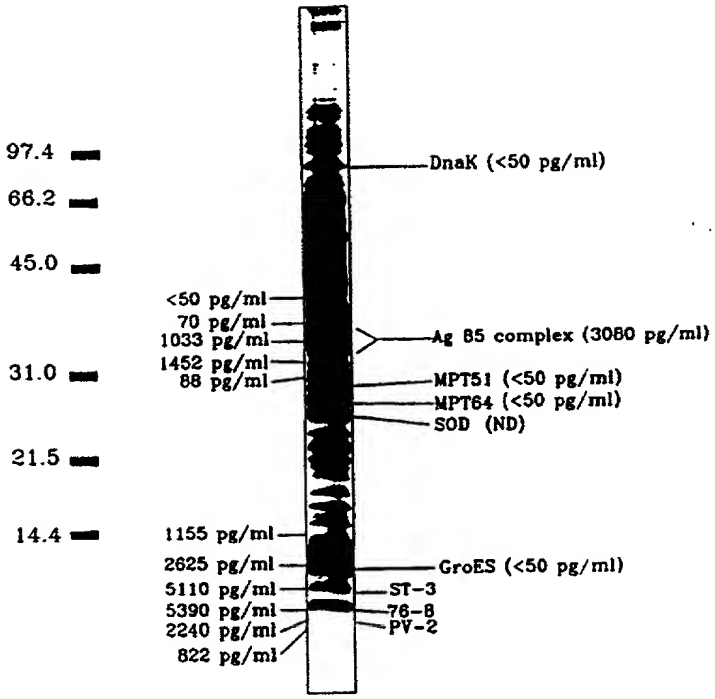
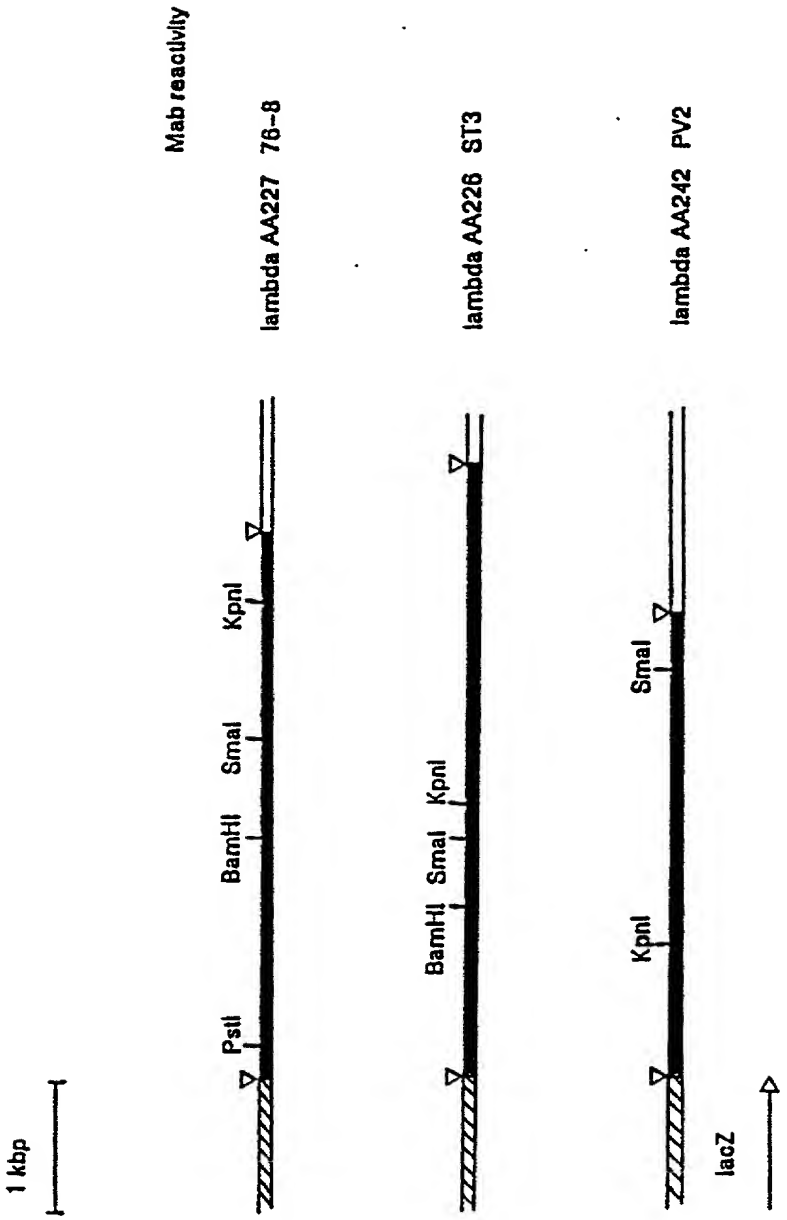

97.4
66.2
45.0
31.0
21.5
14.4
DnaK (<50 pg/ml)
<50 pg/ml
70 pg/ml
1033 pg/ml
1452 pg/ml
88 pg/ml
Ag 85 complex (3080 pg/ml)
MPT51 (<50 pg/ml)
MPT64 (<50 pg/ml)
SOD (ND)
1155 pg/ml
2625 pg/ml
5110 pg/ml
5390 pg/ml
2240 pg/ml
822 pg/ml
GroES (<50 pg/ml)
ST-3
76-8
PV-2

Fig. 6



Physical map of recombinant lambda phages expressing products reactive with Mabs recognizing low M.W. components

Fig. 7

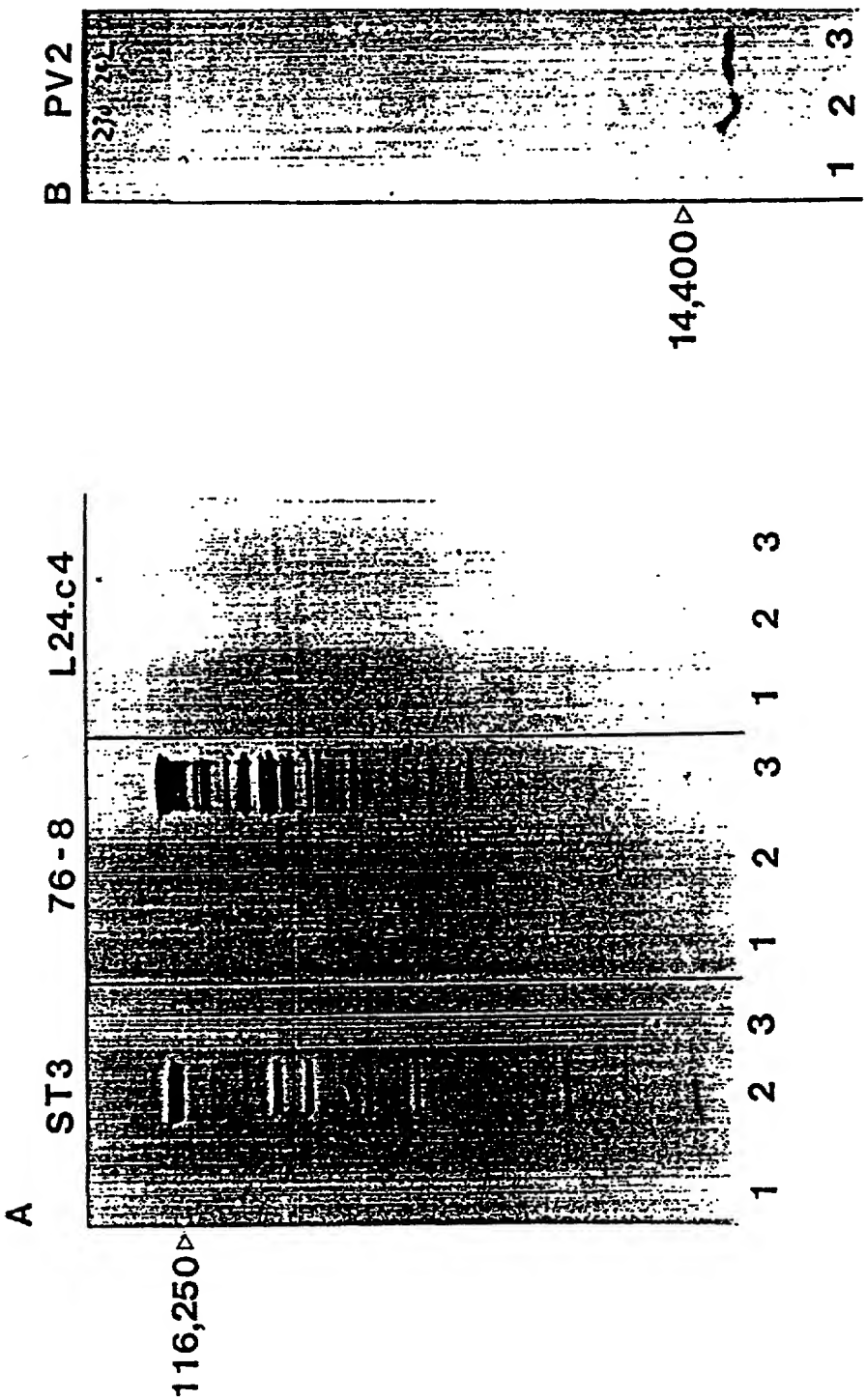


Fig. 8

```
1    GGCCGCCGGT ACCTATGTGG CCGCCGATGC TGCGGNCGCG TCGACCTATA CCGGGTTCTG                        60
                 -35region                         -10 region
61   ATCGAACCCT GCTGACCGAG AGGACTTGTG  ATG TCG CAA ATC ATG TAC AAC TAC CCC GCG             120
                Shine Delgarno          M   S   Q   I   M   Y   N   Y   P   A
121  ATG TTG GGT CAC GCC GGG GAT AAG GCC GGA TAT GCC GGC ACG CTG CAG AGC TTG GGT GCC        180
      M   L   G   H   A   G   D   K   A   G   Y   A   G   T   L   Q   S   L   G   A
181  GAG ATC GCC GTG GAG CAG GCC GCG TTG CAG AGT GCG TGG CAG GGC GAT ACC GGG ATC ACG        240
      E   I   A   V   E   Q   A   A   L   Q   S   A   W   Q   G   D   T   G   I   T
241  TAT CAG GCG TGG CAG GCA CAG TGG AAC CAG GCC ATG GAA GAT TTG GTG CGG GCC TAT CAT        300
      Y   Q   A   W   Q   A   Q   W   N   Q   A   M   E   D   L   V   R   A   Y   H
301  GCG ATG TCC AGC ACC CAT GAA GCC AAC ACC ATG GCG ATG ATG GCC CGC GAC ACC GCC GAA        360
      A   M   S   S   T   H   E   A   N   T   M   A   M   M   A   R   D   T   A   E
361  GCC GCC AAA TGG GGC GGC TAG                                                            381
      A   A   K   W   G   G   •
```

Fig. 9

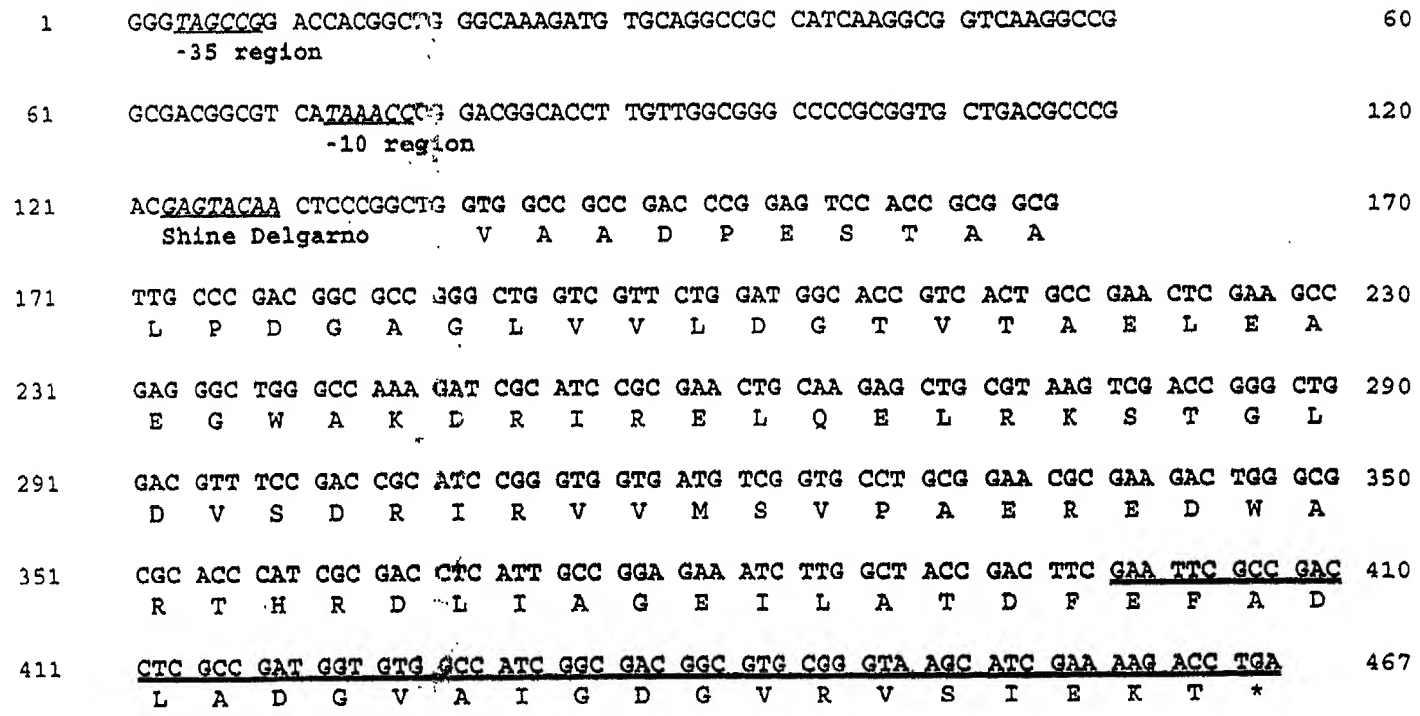

1 GGGTAGCCGG ACCACGGCTG GGCAAAGATG TGCAGGCCGC CATCAAGGCG GTCAAGGCCG 60
-35 region
61 GCGACGGCGT CATAAACCTG GACGGCACCT TGTTGGCGGG CCCCGCGGTG CTGACGCCCG 120
-10 region
121 ACGAGTACAA CTCCCGGCTG GTG GCC GCC GAC CCG GAG TCC ACC GCG GCG 170
Shine Delgarno V A A D P E S T A A
171 TTG CCC GAC GGC GCC GGG CTG GTC GTT CTG GAT GGC ACC GTC ACT GCC GAA CTC GAA GCC 230
L P D G A G L V V L D G T V T A E L E A
231 GAG GGC TGG GCC AAA GAT CGC ATC CGC GAA CTG CAA GAG CTG CGT AAG TCG ACC GGG CTG 290
E G W A K D R I R E L Q E L R K S T G L
291 GAC GTT TCC GAC CGC ATC CGG GTG GTG ATG TCG GTG CCT GCG GAA CGC GAA GAC TGG GCG 350
D V S D R I R V V M S V P A E R E D W A
351 CGC ACC CAT CGC GAC CTC ATT GCC GGA GAA ATC TTG GCT ACC GAC TTC GAA TTC GCC GAC 410
R T H R D L I A G E I L A T D F E F A D
411 CTC GCC GAT GGT GTG GCC ATC GGC GAC GGC GTG CGG GTA AGC ATC GAA AAG ACC TGA 467
L A D G V A I G D G V R V S I E K T *

Fig. 10

```
1   GAATTCGCCGGGTGCACACAGCCTTACACGACGGAGGTGGACACATGAAG   50
                                                 M  K
51  GGTCGGTCGGCGCTGCTGCGGGCGCTCTGGATTGCCGCACTGTCATTCGG  100
      G  R  S  A  L  L  R  A  L  W  I  A  A  L  S  F  G
101 GTTGGGCGGTGTCGCGGTAGCCGCGGAACCCACCGCCAAGGCCGCCCCAT 150
      L  G  G  V  A  V  A  A  E  P  T  A  K  A  A  P
151 ACGAGAACCTGATGGTGCCGTCGCCCTCGATGGGCCGGGACATCCCGGTG 200
      Y  E  N  L  M  V  P  S  P  S  M  G  R  D  I  P  V
201 GCCTTCCTAGCCGGTGGGCCGCACGCGGTGTATCTGCTGGACGCCTTCAA 250
      A  F  L  A  G  G  P  H  A  V  Y  L  L  D  A  F  N
251 CGCCGGCCCGGATGTCAGTAACTGGGTCACCGCGGGTAACGCGATGAACA 300
      A  G  P  D  V  S  N  W  V  T  A  G  N  A  M  N
301 CGTTGGCGGGCAAGGGGATTTCGGTGGTGGCACCGGCCGGTGGTGCGTAC 350
      T  L  A  G  K  G  I  S  V  V  A  P  A  G  G  A  Y
351 AGCATGTACACCAACTGGGAGCAGGATGGCAGCAAGCAGTGGGACACCTT 400
      S  M  Y  T  N  W  E  Q  D  G  S  K  Q  W  D  T  F
401 CTTGTCCGCTGAGCTGCCCGACTGGCTGGCCGCTAACCGGGGCTTGGCCC 450
      L  S  A  E  L  P  D  W  L  A  A  N  R  G  L  A
451 CCGGTGGCCATGCGGCCGTTGGCGCCGCTCAGGGCGGTTACGGGGCGATG 500
      P  G  G  H  A  A  V  G  A  A  Q  G  G  Y  G  A  M
501 GCGCTGGCGGCCTTCCACCCCGACCGCTTCGGCTTCGCTGGCTCGATGTC 550
      A  L  A  A  F  H  P  D  R  F  G  F  A  G  S  M  S
551 GGGCTTTTTGTACCCGTCGAACACCACCACCAACGGTGCGATCGCGGCGG 600
      G  F  L  Y  P  S  N  T  T  T  N  G  A  I  A  A
601 GCATGCAGCAATTCGGCGGTGTGGACACCAACGGAATGTGGGGAGCACCA 650
      G  M  Q  Q  F  G  G  V  D  T  N  G  M  W  G  A  P
651 CAGCTGGGTCGGTGGAAGTGGCACGACCCGTGGGTGCATGCCAGCCTGCT 700
      Q  L  G  R  W  K  W  H  D  P  W  V  H  A  S  L  L
701 GGCGCAAAACAACACCCGGGTGTGGGTGTGGAGCCCGACCAACCCGGGAG 750
      A  Q  N  N  E  R  V  W  V  W  S  P  T  N  P  G
751 CCAGCGATCCCGCCGCCATGATCGGCCAAACCGCCGAGGCGATGGGTAAC 800
      A  S  D  P  A  A  M  I  G  Q  T  A  E  A  M  G  N
801 AGCCGCATGTTCTACAACCAGTATCGCAGCGTCGGCGGGCACAACGGACA 850
      S  R  M  F  Y  N  Q  Y  R  S  V  G  G  H  N  G  H
851 CTTCGACTTCCCAGCCAGCGGTGACAACGGCTGGGGCTCGTGGGCGCCCC 900
      F  D  F  P  A  S  G  D  N  G  W  G  S  W  A  P
901 AGCTGGGCGCTATGTCGGGCGATATCGTCGGTGCGATCCGCTAAGCGAAT 950
      Q  L  G  A  M  S  G  D  I  V  G  A  I  R  .
951 TC                                               952
```

Fig. 11

2-DE reference map of ST-CF

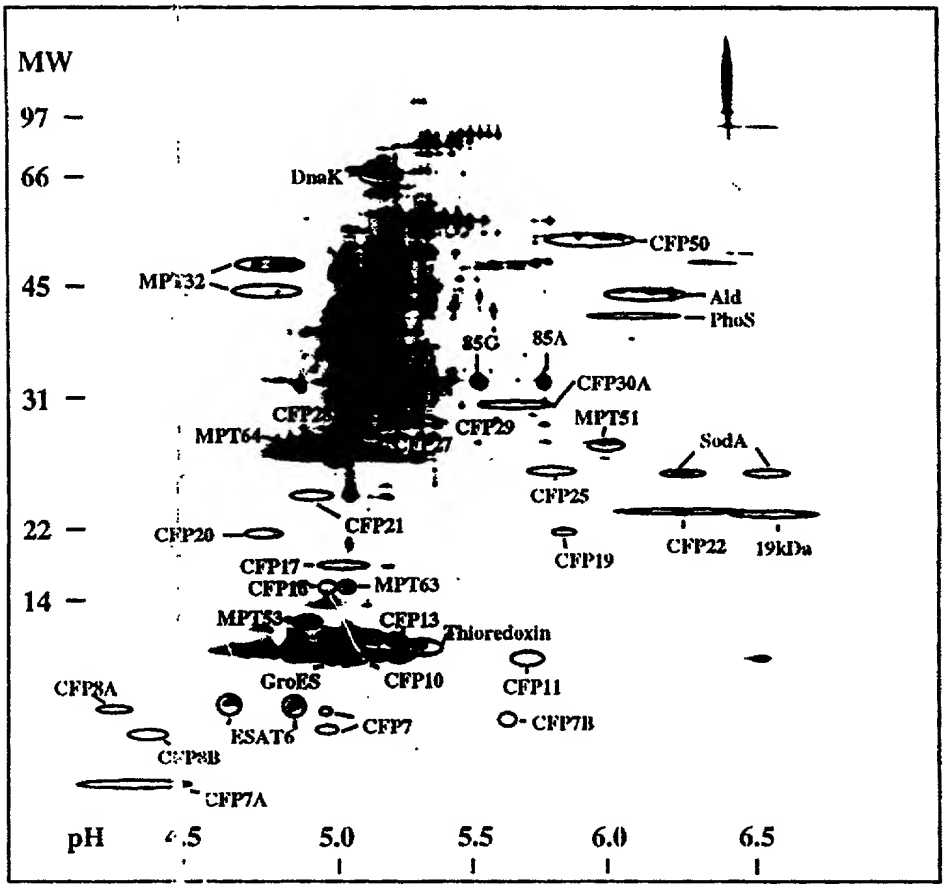


Fig. 12

TB10.4	MSQIMYNYPAMLGHAGDMAGYAGTLQSLGAEIAVEQAALQSAWQGDTGITYQAWQAQWNQAMEDLVRAYHAMSSTHEANTMAMMARDTAEAAKWGG
TB10.4-P1	MSQIMYNYPAMLGHAGDM
TB10.4-P2	MLGHAGDMAGYAGTLQSL
TB10.4-P3	YAGTLQSLGAEIAVEQAA
TB10.4-P4	EIAVEQAALQSAWQGDTG
TB10.4-P5	SAWQGDTGITYQAWQAQW
TB10.4-P6	YQAWQAQWNQAMEDLVRA
TB10.4-P7	AMEDLVRAYHAMSSTHEA
TB10.4-P8	AMSSTHEANTMAMMARDT
TB10.4-P9	MAMMARDTAEAAKWGG

Fig. 13

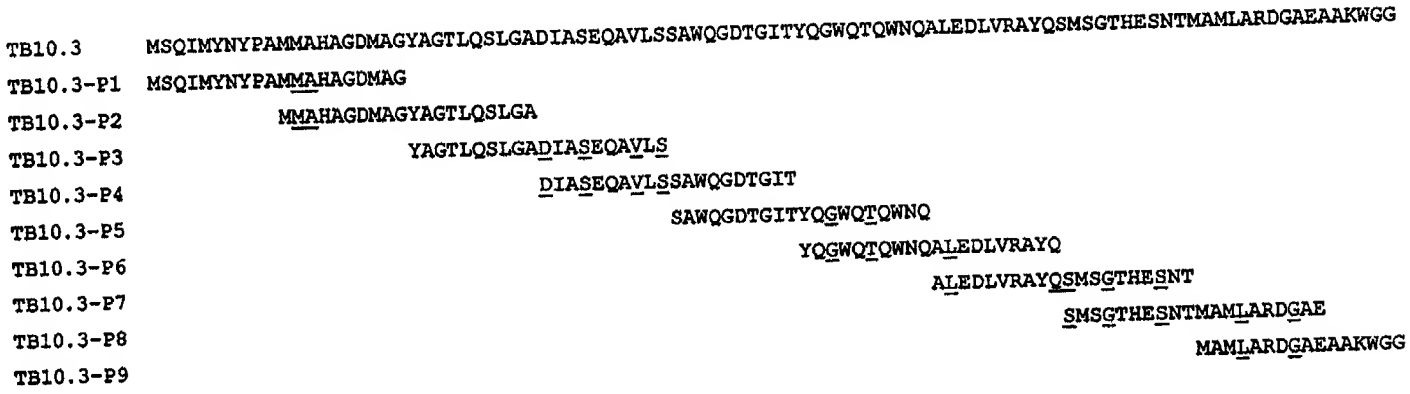

TB10.3 MSQIMYNYPAMMAHAGDMAGYAGTLQSLGADIASEQAVLSSAWQGDTGITYQGWQTQWNQALEDLVRAYQSMSGTHESNTMAMLARDGAEAAKWGG
TB10.3-P1 MSQIMYNYPAMMAHAGDMAG
TB10.3-P2 MMAHAGDMAGYAGTLQSLGA
TB10.3-P3 YAGTLQSLGADIASEQAVLS
TB10.3-P4 DIASEQAVLSSAWQGDTGIT
TB10.3-P5 SAWQGDTGITYQGWQTQWNQ
TB10.3-P6 YQGWQTQWNQALEDLVRAYQ
TB10.3-P7 ALEDLVRAYQSMSGTHESNT
TB10.3-P8 SMSGTHESNTMAMLARDGAE
TB10.3-P9 MAMLARDGAEAAKWGG

Fig. 14

TB12.9	MSQSMYSYPAMTANVGDMAGYTGTTQSLGADIASERTAPSRACQGDLGMSHQDWQAQWNQAMEALARAYRRCRRALRQIGVLERPVGDSSDCGTIRVGSFRGRWLDPRHAGPATAADAGD
TB12.9-P1	MSQSMYSYPAMTANVGDMAG
TB12.9-P2	MTANVGDMAGYTGTTQSLGA
TB12.9-P3	YTGTTQSLGADIASERTAPS
TB12.9-P4	DIASERTAPSRACQGDLGMS
TB12.9-P5	RACQGDLGMSHQDWQAQWNQ
TB12.9-P6	HQDWQAQWNQAMEALARAYR
TB12.9-P7	AMEALARAYRRCRRALRQIG
TB12.9-P8	RCRRALRQIGVLERPVGDSS
TB12.9-P9	VLERPVGDSSDCGTIRVGSF
TB12.9-P10	DCGTIRVGSFRGRWLDPRHA
TB12.9-P11	RGRWLDPRHAGPATAADAGD

Fig. 15